STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: 10 579,137

Source: Trust

Date Processed by STIC: 5-24-06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER
VERSION 4.4.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
       http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
<u>Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:</u>

1. EFS-Bio <u>(<http://www.uspto.gov/ebc/efs/downloads/documents.htm></u> , **EFS Submission
   User Manual - ePAVE)**
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street,
   Alexandria, VA 22314

Revised 01/10/06

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: 10/579,137

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
   Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
   prevent "wrapping."

2 _____ Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
   Numbering   use space characters, instead.

4 _____ Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
   ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length   Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules,
   each n or Xaa can only represent a single residue. Please present the maximum number of each
   residue having variable length and indicate in the <220><223> section that some may be missing.

6 _____ PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220><223> section to be missing from amino acid
   "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
   previously coded nucleic acid sequence. Please manually copy the relevant <220><223> section to
   the subsequent amino acid sequence. This applies to the mandatory <220><223> sections for
   Artificial or Unknown sequences.

7 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
   (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
   (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
   (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
   This sequence is intentionally skipped

   Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
   (NEW RULES)   <210> sequence id number
   <400> sequence id number
   000

9 _____ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
   (NEW RULES)   Per 1.823 of Sequence Rules, use of <220><223> is MANDATORY if n's or Xaa's are present.
   In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
   Response   scientific name (Genus/species). <220><223> section is required when <213> response is Unknown or
   is Artificial Sequence

11 _____ Use of <220>   Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
   "Unknown." Please explain source of genetic material in <220> to <223> section.
   (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
   "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
   listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n/Xaa   "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC – Biotechnology Systems Branch – 09/09/2003

RAW SEQUENCE LISTING   DATE: 05/24/2006
PATENT APPLICATION: US/10/579,137 TIME: 12:20:34

Input Set : A:\TUR-181.Sequence.ST25.txt
Output Set: N:\CRF4\05242006\J579137.raw

```
   3 <110> APPLICANT: Abacus Diagnostica Oy
   4        NURMI, Jussi
   5        KORPIMAKI, Teemu
   7 <120> TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION ASSAY AND ARRANGEMENT
THEREFOR
   9 <130> FILE REFERENCE: TUR-181
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/579,137
C--> 12 <141> CURRENT FILING DATE: 2006-05-15
  14 <150> PRIOR APPLICATION NUMBER: US 60/520,647
  15 <151> PRIOR FILING DATE: 2003-11-18
  17 <150> PRIOR APPLICATION NUMBER: FI 20031678
  18 <151> PRIOR FILING DATE: 2003-11-18
  20 <160> NUMBER OF SEQ ID NOS: 10
  22 <170> SOFTWARE: PatentIn version 3.2
  24 <210> SEQ ID NO: 1
  25 <211> LENGTH: 28
  26 <212> TYPE: DNA
  27 <213> ORGANISM: Artificial Sequence
  29 <220> FEATURE:
  30 <223> OTHER INFORMATION: Probe
  32 <400> SEQUENCE: 1
  33 cgatttcatc cgcgtgtttc ttttcgta                              28
  36 <210> SEQ ID NO: 2
  37 <211> LENGTH: 14
  38 <212> TYPE: DNA
  39 <213> ORGANISM: Artificial Sequence
  41 <220> FEATURE:
  42 <223> OTHER INFORMATION: quencher
  44 <400> SEQUENCE: 2
  45 cgcggatgaa atcg                                             14
  48 <210> SEQ ID NO: 3
  49 <211> LENGTH: 19
  50 <212> TYPE: DNA
  51 <213> ORGANISM: Artificial Sequence
  53 <220> FEATURE:
  54 <223> OTHER INFORMATION: primer
  56 <400> SEQUENCE: 3
  57 tgcaagtcct aagacgcca                                        19
  60 <210> SEQ ID NO: 4
  61 <211> LENGTH: 24
  62 <212> TYPE: DNA
  63 <213> ORGANISM: Artificial Sequence
  65 <220> FEATURE:
  66 <223> OTHER INFORMATION: primer
```

Does Not Comply
Corrected Diskette Needed

(Pg. 1-2)

What is the source of genetic material?

See item #11 on error summary sheet.

```
 68 <400> SEQUENCE: 4
 69 cactgcatct ccgtggtata ctaa                                    24
 72 <210> SEQ ID NO: 5
 73 <211> LENGTH: 22
 74 <212> TYPE: DNA
 75 <213> ORGANISM: Artificial Sequence
 77 <220> FEATURE:
 78 <223> OTHER INFORMATION: probe
 80 <400> SEQUENCE: 5
 81 ttgatgtgat ggctcctggc ca
 84 <210> SEQ ID NO: 6
 85 <211> LENGTH: 12
 86 <212> TYPE: DNA
 87 <213> ORGANISM: Artificial Sequence
 89 <220> FEATURE:
 90 <223> OTHER INFORMATION: quencher
 92 <400> SEQUENCE: 6
 93 ccatcacatc aa
 96 <210> SEQ ID NO: 7
 97 <211> LENGTH: 20
 98 <212> TYPE: DNA
 99 <213> ORGANISM: Artificial Sequence
101 <220> FEATURE:
102 <223> OTHER INFORMATION: primer
104 <400> SEQUENCE: 7
105 atggatgtta tcaacatgag
108 <210> SEQ ID NO: 8
109 <211> LENGTH: 18
110 <212> TYPE: DNA
111 <213> ORGANISM: Artificial Sequence
113 <220> FEATURE:
114 <223> OTHER INFORMATION: primer
116 <400> SEQUENCE: 8
117 gagtcgccat ggacgttc
120 <210> SEQ ID NO: 9
121 <211> LENGTH: 20
122 <212> TYPE: DNA
123 <213> ORGANISM: Artificial Sequence
125 <220> FEATURE:
126 <223> OTHER INFORMATION: primer
128 <400> SEQUENCE: 9
129 tgaagtctga cgtggacatc
132 <210> SEQ ID NO: 10
133 <211> LENGTH: 21
134 <212> TYPE: DNA
135 <213> ORGANISM: Artificial Sequence
137 <220> FEATURE:
138 <223> OTHER INFORMATION: primer
140 <400> SEQUENCE: 10
```

(Handwritten annotations:) What is the source of Genetic material? = Invalid Response

22

12

← See item #11 on error Summary Sheet.

20

20

      141 cttgatcttc attgtgctgg g   21

Input Set : A:\TUR-181.Sequence.ST25.txt
Output Set: N:\CRF4\05242006\J579137.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application
Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date